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Application No: 09042460 Version No: 1.0

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Total Warnings: 0

Total Errors: 0

No. of SeqIDs Defined: 101

Actual SeqID Count: 101

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Morin, Gregg B.
Allsopp, Richard
DePinho, Ronald
Greenberg, Roger

(ii) TITLE OF INVENTION: Mouse Telomerase Reverse Transcriptase

(iii) NUMBER OF SEQUENCES: 101

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Townsend and Townsend and Crew LLP
(B) STREET: Two Embarcadero Center, Eighth Floor
(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94111-3834

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09042460
(B) FILING DATE: 1998-03-16

(vii) PRIOR APPLICATION DATA:

(B) FILING DATE: 16-MAR-1998
(C) CLASSIFICATION: 536

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/724,643
(B) FILING DATE: 01-OCT-1996

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/844,419
(B) FILING DATE: 18-APR-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/846,017
(B) FILING DATE: 25-APR-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/851,843
(B) FILING DATE: 06-MAY-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/854,050

(B) FILING DATE: 09-MAY-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/911,312

(B) FILING DATE: 14-AUG-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/912,951

(B) FILING DATE: 14-AUG-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/915,503

(B) FILING DATE: 14-AUG-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: WO PCT/US97/17618

(B) FILING DATE: 01-OCT-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: WO PCT/US97/17885

(B) FILING DATE: 01-OCT-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/974,549

(B) FILING DATE: 19-NOV-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/974,584

(B) FILING DATE: 19-NOV-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/979,742

(B) FILING DATE: 26-NOV-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Einhorn, Gregory P.

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(C) REFERENCE/DOCKET NUMBER: 015389-003110US

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3496 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
 (B) LOCATION: 1..3496
 (D) OTHER INFORMATION: /note= "mouse telomerase reverse
 transcriptase (mTRT) cDNA clone"

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION: 10..3435
 (D) OTHER INFORMATION: /note= "mouse telomerase reverse
 transcriptase (mTRT) cDNA"

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 39..3404
 (D) OTHER INFORMATION: /product= "mouse telomerase reverse
 transcriptase (mTRT) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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1 5	
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Arg Cys Pro Ala Val Arg Ser Leu Leu Arg Ser Arg Tyr Arg Glu Val	
10 15 20	
TGG CCG CTG GCA ACC TTT GTG CGG CGC CTG GGG CCC GAG GGC AGG CGG	149
Trp Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro Glu Gly Arg Arg	
25 30 35	
CTT GTG CAA CCC GGG GAC CCG AAG ATC TAC CGC ACT TTG GTT GCC CAA	197
Leu Val Gln Pro Gly Asp Pro Lys Ile Tyr Arg Thr Leu Val Ala Gln	
40 45 50	
TGC CTA GTG TGC ATG CAC TGG GGC TCA CAG CCT CCA CCT GCC GAC CTT	245
Cys Leu Val Cys Met His Trp Gly Ser Gln Pro Pro Pro Ala Asp Leu	
55 60 65	
TCC TTC CAC CAG GTG TCA TCC CTG AAA GAG CTG GTG GCC AGG GTT GTG	293
Ser Phe His Gln Val Ser Ser Leu Lys Glu Leu Val Ala Arg Val Val	
70 75 80 85	
CAG AGA CTC TGC GAG CGC AAC GAG AGA AAC GTG CTG GCT TTT GGC TTT	341
Gln Arg Leu Cys Glu Arg Asn Glu Arg Asn Val Leu Ala Phe Gly Phe	
90 95 100	
GAG CTG CTT AAC GAG GCC AGA GGC GGG CCT CCC ATG GCC TTC ACT AGT	389
Glu Leu Leu Asn Glu Ala Arg Gly Gly Pro Pro Met Ala Phe Thr Ser	
105 110 115	
AGC GTG CGT AGC TAC TTG CCC AAC ACT GTT ATT GAG ACC CTG CGT GTC	437
Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Ile Glu Thr Leu Arg Val	
120 125 130	
AGT GGT GCA TGG ATG CTA CTG TTG AGC CGA GTG GGC GAC GAC CTG CTG	485

Ser Gly Ala Trp Met Leu Leu Leu Ser Arg Val Gly Asp Asp Leu Leu	
135 140 145	
GTC TAC CTG CTG GCA CAC TGT GCT CTT TAT CTT CTG GTG CCC CCC AGC	533
Val Tyr Leu Leu Ala His Cys Ala Leu Tyr Leu Leu Val Pro Pro Ser	
150 155 160 165	
TGT GCC TAC CAG GTG TGT GGG TCT CCC CTG TAC CAA ATT TGT GCC ACC	581
Cys Ala Tyr Gln Val Cys Gly Ser Pro Leu Tyr Gln Ile Cys Ala Thr	
170 175 180	
ACG GAT ATC TGG CCC TCT GTG TCC GCT AGT TAC AGG CCC ACC CGA CCC	629
Thr Asp Ile Trp Pro Ser Val Ser Ala Ser Tyr Arg Pro Thr Arg Pro	
185 190 195	
GTG GGC AGG AAT TTC ACT AAC CTT AGG TTC TTA CAA CAG ATC AAG AGC	677
Val Gly Arg Asn Phe Thr Asn Leu Arg Phe Leu Gln Gln Ile Lys Ser	
200 205 210	
AGT AGT CGC CAG GAA GCA CCG AAA CCC CTG GCC TTG CCA TCT CGA GGT	725
Ser Ser Arg Gln Glu Ala Pro Lys Pro Leu Ala Leu Pro Ser Arg Gly	
215 220 225	
ACA AAG AGG CAT CTG AGT CTC ACC AGT ACA AGT GTG CCT TCA GCT AAG	773
Thr Lys Arg His Leu Ser Leu Thr Ser Thr Ser Val Pro Ser Ala Lys	
230 235 240 245	
AAG GCC AGA TGC TAT CCT GTC CCG AGA GTG GAG GAG GGA CCC CAC AGG	821
Lys Ala Arg Cys Tyr Pro Val Pro Arg Val Glu Glu Gly Pro His Arg	
250 255 260	
CAG GTG CTA CCA ACC CCA TCA GGC AAA TCA TGG GTG CCA AGT CCT GCT	869
Gln Val Leu Pro Thr Pro Ser Gly Lys Ser Trp Val Pro Ser Pro Ala	
265 270 275	
CGG TCC CCC GAG GTG CCT ACT GCA GAG AAA GAT TTG TCT TCT AAA GGA	917
Arg Ser Pro Glu Val Pro Thr Ala Glu Lys Asp Leu Ser Ser Lys Gly	
280 285 290	
AAG GTG TCT GAC CTG AGT CTC TCT GGG TCG GTG TGC TGT AAA CAC AAG	965
Lys Val Ser Asp Leu Ser Leu Ser Gly Ser Val Cys Cys Lys His Lys	
295 300 305	
CCC AGC TCC ACA TCT CTG CTG TCA CCA CCC CGC CAA AAT GCC TTT CAG	1013
Pro Ser Ser Thr Ser Leu Leu Ser Pro Pro Arg Gln Asn Ala Phe Gln	
310 315 320 325	
CTC AGG CCA TTT ATT GAG ACC AGA CAT TTC CTT TAC TCC AGG GGA GAT	1061
Leu Arg Pro Phe Ile Glu Thr Arg His Phe Leu Tyr Ser Arg Gly Asp	
330 335 340	
GGC CAA GAG CGT CTA AAC CCC TCA TTC CTA CTC AGC AAC CTC CAG CCT	1109
Gly Gln Glu Arg Leu Asn Pro Ser Phe Leu Leu Ser Asn Leu Gln Pro	
345 350 355	
AAC TTG ACT GGG GCC AGG AGA CTG GTG GAG ATC ATC TTT CTG GGC TCA	1157
Asn Leu Thr Gly Ala Arg Arg Leu Val Glu Ile Ile Phe Leu Gly Ser	

360	365	370	
AGG CCT AGG ACA TCA GGA CCA CTC TGC AGG ACA CAC CGT CTA TCG CGT			1205
Arg Pro Arg Thr Ser Gly Pro Leu Cys Arg Thr His Arg Leu Ser Arg			
375	380	385	
CGA TAC TGG CAG ATG CGG CCC CTG TTC CAA CAG CTG CTG GTG AAC CAT			1253
Arg Tyr Trp Gln Met Arg Pro Leu Phe Gln Gln Leu Leu Val Asn His			
390	395	400	405
GCA GAG TGC CAA TAT GTC AGA CTC CTC AGG TCA CAT TGC AGG TTT CGA			1301
Ala Glu Cys Gln Tyr Val Arg Leu Leu Arg Ser His Cys Arg Phe Arg			
410	415	420	
ACA GCA AAC CAA CAG GTG ACA GAT GCC TTG AAC ACC AGC CCA CCG CAC			1349
Thr Ala Asn Gln Gln Val Thr Asp Ala Leu Asn Thr Ser Pro Pro His			
425	430	435	
CTC ATG GAT TTG CTC CGC CTG CAC AGC AGT CCC TGG CAG GTA TAT GGT			1397
Leu Met Asp Leu Leu Arg Leu His Ser Ser Pro Trp Gln Val Tyr Gly			
440	445	450	
TTT CTT CGG GCC TGT CTC TGC AAG GTG GTG TCT GCT AGT CTC TGG GGT			1445
Phe Leu Arg Ala Cys Leu Cys Lys Val Val Ser Ala Ser Leu Trp Gly			
455	460	465	
ACC AGG CAC AAT GAG CGC CGC TTC TTT AAG AAC TTA AAG AAG TTC ATC			1493
Thr Arg His Asn Glu Arg Arg Phe Phe Lys Asn Leu Lys Lys Phe Ile			
470	475	480	485
TCG TTG GGG AAA TAC GGC AAG CTA TCA CTG CAG GAA CTG ATG TGG AAG			1541
Ser Leu Gly Lys Tyr Gly Lys Leu Ser Leu Gln Glu Leu Met Trp Lys			
490	495	500	
ATG AAA GTA GAG GAT TGC CAC TGG CTC CGC AGC AGC CCG GGG AAG GAC			1589
Met Lys Val Glu Asp Cys His Trp Leu Arg Ser Ser Pro Gly Lys Asp			
505	510	515	
CGT GTC CCC GCT GCA GAG CAC CGT CTG AGG GAG AGG ATC CTG GCT ACG			1637
Arg Val Pro Ala Ala Glu His Arg Leu Arg Glu Arg Ile Leu Ala Thr			
520	525	530	
TTC CTG TTC TGG CTG ATG GAC ACA TAC GTG GTA CAG CTG CTT AGG TCA			1685
Phe Leu Phe Trp Leu Met Asp Thr Tyr Val Val Gln Leu Leu Arg Ser			
535	540	545	
TTC TTT TAC ATC ACA GAG AGC ACA TTC CAG AAG AAC AGG CTC TTC TTC			1733
Phe Phe Tyr Ile Thr Glu Ser Thr Phe Gln Lys Asn Arg Leu Phe Phe			
550	555	560	565
TAC CGT AAG AGT GTG TGG AGC AAG CTG CAG AGC ATT GGA GTC AGG CAA			1781
Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Val Arg Gln			
570	575	580	
CAC CTT GAG AGA GTG CGG CTA CGG GAG CTG TCA CAA GAG GAG GTC AGG			1829
His Leu Glu Arg Val Arg Leu Arg Glu Leu Ser Gln Glu Glu Val Arg			
585	590	595	

CAT CAC CAG GAC ACC TGG CTA GCC ATG CCC ATC TGC AGA CTG CGC TTC	1877
His His Gln Asp Thr Trp Leu Ala Met Pro Ile Cys Arg Leu Arg Phe	
600 605 610	
ATC CCC AAG CCC AAC GGC CTG CGG CCC ATT GTG AAC ATG AGT TAT AGC	1925
Ile Pro Lys Pro Asn Gly Leu Arg Pro Ile Val Asn Met Ser Tyr Ser	
615 620 625	
ATG GGT ACC AGA GCT TTG GGC AGA AGG AAG CAG GCC CAG CAT TTC ACC	1973
Met Gly Thr Arg Ala Leu Gly Arg Arg Lys Gln Ala Gln His Phe Thr	
630 635 640 645	
CAG CGT CTC AAG ACT CTC TTC AGC ATG CTC AAC TAT GAG CGG ACA AAA	2021
Gln Arg Leu Lys Thr Leu Phe Ser Met Leu Asn Tyr Glu Arg Thr Lys	
650 655 660	
CAT CCT CAC CTT ATG GGG TCT TCT GTA CTG GGT ATG AAT GAC ATC TAC	2069
His Pro His Leu Met Gly Ser Ser Val Leu Gly Met Asn Asp Ile Tyr	
665 670 675	
AGG ACC TGG CGG GCC TTT GTG CTG CGT GTG CGT GCT CTG GAC CAG ACA	2117
Arg Thr Trp Arg Ala Phe Val Leu Arg Val Arg Ala Leu Asp Gln Thr	
680 685 690	
CCC AGG ATG TAC TTT GTT AAG GCA GAT GTG ACC GGG GCC TAT GAT GCC	2165
Pro Arg Met Tyr Phe Val Lys Ala Asp Val Thr Gly Ala Tyr Asp Ala	
695 700 705	
ATC CCC CAG GGT AAG CTG GTG GAG GTT GTT GCC AAT ATG ATC AGG CAC	2213
Ile Pro Gln Gly Lys Leu Val Glu Val Val Ala Asn Met Ile Arg His	
710 715 720 725	
TCG GAG AGC ACG TAC TGT ATC CGC CAG TAT GCA GTG GTC CGG AGA GAT	2261
Ser Glu Ser Thr Tyr Cys Ile Arg Gln Tyr Ala Val Val Arg Arg Asp	
730 735 740	
AGC CAA GGC CAA GTC CAC AAG TCC TTT AGG AGA CAG GTC ACC ACC CTC	2309
Ser Gln Gly Gln Val His Lys Ser Phe Arg Arg Gln Val Thr Thr Leu	
745 750 755	
TCT GAC CTC CAG CCA TAC ATG GGC CAG TTC CTT AAG CAT CTG CAG GAT	2357
Ser Asp Leu Gln Pro Tyr Met Gly Gln Phe Leu Lys His Leu Gln Asp	
760 765 770	
TCA GAT GCC AGT GCA CTG AGG AAC TCC GTT GTC ATC GAG CAG AGC ATC	2405
Ser Asp Ala Ser Ala Leu Arg Asn Ser Val Val Ile Glu Gln Ser Ile	
775 780 785	
TCT ATG AAT GAG AGC AGC AGC AGC CTG TTT GAC TTC TTC CTG CAC TTC	2453
Ser Met Asn Glu Ser Ser Ser Ser Leu Phe Asp Phe Phe Leu His Phe	
790 795 800 805	
CTG CGT CAC AGT GTC GTA AAG ATT GGT GAC AGG TGC TAT ACG CAG TGC	2501
Leu Arg His Ser Val Val Lys Ile Gly Asp Arg Cys Tyr Thr Gln Cys	
810 815 820	

CAG GGC ATC CCC CAG GGC TCC AGC CTA TCC ACC CTG CTC TGC AGT CTG	2549
Gln Gly Ile Pro Gln Gly Ser Ser Leu Ser Thr Leu Leu Cys Ser Leu	
825 830 835	
TGT TTC GGA GAC ATG GAG AAC AAG CTG TTT GCT GAG GTG CAG CGG GAT	2597
Cys Phe Gly Asp Met Glu Asn Lys Leu Phe Ala Glu Val Gln Arg Asp	
840 845 850	
GGG TTG CTT TTA CGT TTT GTT GAT GAC TTT CTG TTG GTG ACG CCT CAC	2645
Gly Leu Leu Leu Arg Phe Val Asp Asp Phe Leu Leu Val Thr Pro His	
855 860 865	
TTG GAC CAA GCA AAA ACC TTC CTC AGC ACC CTG GTC CAT GGC GTT CCT	2693
Leu Asp Gln Ala Lys Thr Phe Leu Ser Thr Leu Val His Gly Val Pro	
870 875 880 885	
GAG TAT GGG TGC ATG ATA AAC TTG CAG AAG ACA GTG GTG AAC TTC CCT	2741
Glu Tyr Gly Cys Met Ile Asn Leu Gln Lys Thr Val Val Asn Phe Pro	
890 895 900	
GTG GAG CCT GGT ACC CTG GGT GGT GCA GCT CCA TAC CAG CTG CCT GCT	2789
Val Glu Pro Gly Thr Leu Gly Gly Ala Ala Pro Tyr Gln Leu Pro Ala	
905 910 915	
CAC TGC CTG TTT CCC TGG TGT GGC TTG CTG CTG GAC ACT CAG ACT TTG	2837
His Cys Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Gln Thr Leu	
920 925 930	
GAG GTG TTC TGT GAC TAC TCA GGT TAT GCC CAG ACC TCA ATT AAG ACG	2885
Glu Val Phe Cys Asp Tyr Ser Gly Tyr Ala Gln Thr Ser Ile Lys Thr	
935 940 945	
AGC CTC ACC TTC CAG AGT GTC TTC AAA GCT GGG AAG ACC ATG CGG AAC	2933
Ser Leu Thr Phe Gln Ser Val Phe Lys Ala Gly Lys Thr Met Arg Asn	
950 955 960 965	
AAG CTC CTG TCG GTC TTG CGG TTG AAG TGT CAC GGT CTA TTT CTA GAC	2981
Lys Leu Leu Ser Val Leu Arg Leu Lys Cys His Gly Leu Phe Leu Asp	
970 975 980	
TTG CAG GTG AAC AGC CTC CAG ACA GTC TGC ATC AAT ATA TAC AAG ATC	3029
Leu Gln Val Asn Ser Leu Gln Thr Val Cys Ile Asn Ile Tyr Lys Ile	
985 990 995	
TTC CTG CTT CAG GCC TAC AGG TTC CAT GCA TGT GTG ATT CAG CTT CCC	3077
Phe Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Ile Gln Leu Pro	
1000 1005 1010	
TTT GAC CAG CGT GTT AGG AAG AAC CTC ACA TTC TTT CTG GGC ATC ATC	3125
Phe Asp Gln Arg Val Arg Lys Asn Leu Thr Phe Phe Leu Gly Ile Ile	
1015 1020 1025	
TCC AGC CAA GCA TCC TGC TGC TAT GCT ATC CTG AAG GTC AAG AAT CCA	3173
Ser Ser Gln Ala Ser Cys Cys Tyr Ala Ile Leu Lys Val Lys Asn Pro	
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GGA ATG ACA CTA AAG GCC TCT GGC TCC TTT CCT CCT GAA GCC GCA CAT	3221

Gly Met Thr Leu Lys Ala Ser Gly Ser Phe Pro Pro Glu Ala Ala His	
1050 1055 1060	
TGG CTC TGC TAC CAG GCC TTC CTG CTC AAG CTG GCT GCT CAT TCT GTC	3269
Trp Leu Cys Tyr Gln Ala Phe Leu Leu Lys Leu Ala Ala His Ser Val	
1065 1070 1075	
ATC TAC AAA TGT CTC CTG GGA CCT CTG AGG ACA GCC CAA AAA CTG CTG	3317
Ile Tyr Lys Cys Leu Leu Gly Pro Leu Arg Thr Ala Gln Lys Leu Leu	
1080 1085 1090	
TGC CGG AAG CTC CCA GAG GCG ACA ATG ACC ATC CTT AAA GCT GCA GCT	3365
Cys Arg Lys Leu Pro Glu Ala Thr Met Thr Ile Leu Lys Ala Ala Ala	
1095 1100 1105	
GAC CCA GCC CTA AGC ACA GAC TTT CAG ACC ATT TTG GAC TAACCCTGTC	3414
Asp Pro Ala Leu Ser Thr Asp Phe Gln Thr Ile Leu Asp	
1110 1115 1120	
TCCTTCCGCT AGATGAACAT GAAGGGCGAA TTCCAGCACA CTGGCGGCCG TTAGTAGTGG	3474
ATCCGAGCTC GGTACCAAGC TT	3496

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1122 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Arg Ala Pro Arg Cys Pro Ala Val Arg Ser Leu Leu Arg Ser	
1 5 10 15	
Arg Tyr Arg Glu Val Trp Pro Leu Ala Thr Phe Val Arg Arg Leu Gly	
20 25 30	
Pro Glu Gly Arg Arg Leu Val Gln Pro Gly Asp Pro Lys Ile Tyr Arg	
35 40 45	
Thr Leu Val Ala Gln Cys Leu Val Cys Met His Trp Gly Ser Gln Pro	
50 55 60	
Pro Pro Ala Asp Leu Ser Phe His Gln Val Ser Ser Leu Lys Glu Leu	
65 70 75 80	
Val Ala Arg Val Val Gln Arg Leu Cys Glu Arg Asn Glu Arg Asn Val	
85 90 95	
Leu Ala Phe Gly Phe Glu Leu Leu Asn Glu Ala Arg Gly Gly Pro Pro	
100 105 110	
Met Ala Phe Thr Ser Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Ile	

115

120

125

Glu Thr Leu Arg Val Ser Gly Ala Trp Met Leu Leu Leu Ser Arg Val
130 135 140

Gly Asp Asp Leu Leu Val Tyr Leu Leu Ala His Cys Ala Leu Tyr Leu
145 150 155 160

Leu Val Pro Pro Ser Cys Ala Tyr Gln Val Cys Gly Ser Pro Leu Tyr
165 170 175

Gln Ile Cys Ala Thr Thr Asp Ile Trp Pro Ser Val Ser Ala Ser Tyr
180 185 190

Arg Pro Thr Arg Pro Val Gly Arg Asn Phe Thr Asn Leu Arg Phe Leu
195 200 205

Gln Gln Ile Lys Ser Ser Ser Arg Gln Glu Ala Pro Lys Pro Leu Ala
210 215 220

Leu Pro Ser Arg Gly Thr Lys Arg His Leu Ser Leu Thr Ser Thr Ser
225 230 235 240

Val Pro Ser Ala Lys Lys Ala Arg Cys Tyr Pro Val Pro Arg